

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2002, 03:45:21 ; Search time 1604.32 Seconds  
(without alignments)  
9018.610 Million cell updates/sec

Title: US-09-811-118-2  
Perfect score: 1072  
Sequence: 1 GACGCCGCCACCTCCGAC.....TTGCATCCACATGAAATTC 1072

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 13736207 segs, 6748477542 residues  
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estcov:\*  
6: em\_estcpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description       |
|------------|-------|-------------|-----------|----|-------------------|
| 1          | 964.8 | 90.0        | 1011      | 9  | AL543692 AL543692 |
| 2          | 840.2 | 78.4        | 961       | 9  | AL543655 AL543655 |
| 3          | 817.2 | 76.2        | 894       | 10 | BI767772 BI767772 |
| 4          | 741.4 | 69.2        | 936       | 10 | BI905842 BI905842 |
| 5          | 737.2 | 68.8        | 846       | 10 | BI561449 BI561449 |
| 6          | 721.6 | 67.3        | 760       | 10 | BI550170 BI550170 |
| 7          | 687.4 | 64.1        | 852       | 9  | AL554204 AL554204 |
| 8          | 653.6 | 61.0        | 720       | 10 | BI772530 BI772530 |
| 9          | 607   | 56.6        | 773       | 9  | AL554203 AL554203 |
| 10         | 600.8 | 56.0        | 617       | 10 | BE383506 BE383506 |
| 11         | 556.2 | 51.9        | 907       | 9  | AL576668 AL576668 |
| 12         | 555.8 | 49.5        | 625       | 9  | AW957082 AW957082 |
| 13         | 530.8 | 47.6        | 534       | 10 | BE314194 BE314194 |
| 14         | 510.8 | 47.6        | 542       | 9  | AW959644 AW959644 |
| 15         | 482.4 | 45.0        | 519       | 9  | AA066605 AA066605 |
| 16         | 473.4 | 44.2        | 664       | 10 | BF965615 BF965615 |
| 17         |       |             | 821       | 10 | BF673639 BF673639 |

|      |       |      |      |    |          |                    |
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| c 18 | 459.4 | 42.9 | 465  | 9  | AI925364 | AI925364 wn53c04.x |
| c 19 | 457.6 | 42.7 | 1042 | 11 | AK014199 | AK014199 Mus muscu |
| c 20 | 453.4 | 42.3 | 466  | 9  | AA599283 | AA599283 ag35b03.s |
| c 21 | 452   | 42.2 | 466  | 9  | AI635816 | AI635816 t281c10.x |
| c 22 | 450.8 | 42.1 | 617  | 9  | BB658193 | BB658193 BB658193  |
| c 23 | 449.8 | 42.0 | 678  | 9  | AW142311 | AW142311 EST292556 |
| c 24 | 447.8 | 41.8 | 675  | 9  | AW141464 | AW141464 EST291514 |
| c 25 | 447.4 | 41.7 | 466  | 9  | AI332841 | AI332841 qp96q11.x |
| c 26 | 446   | 41.6 | 464  | 9  | AW576111 | AW576111 UI-HF-BLO |
| c 27 | 441   | 41.1 | 562  | 9  | AV602925 | AV602925 UI-HF-BLO |
| c 28 | 438   | 40.9 | 885  | 10 | BI453803 | BI453803 603175068 |
| c 29 | 434.4 | 40.5 | 436  | 9  | AA557291 | AA557291 n176b12.s |
| c 30 | 433.8 | 40.5 | 450  | 9  | AA815259 | AA815259 a164d10.s |
| c 31 | 432.2 | 40.3 | 454  | 10 | BE646653 | BE646653 7e91h09.x |
| c 32 | 424.4 | 39.6 | 453  | 9  | AI093865 | AI093865 gq30e01.s |
| c 33 | 423.4 | 39.5 | 436  | 9  | AI094047 | AI094047 qd38f09.s |
| c 34 | 422.8 | 39.4 | 426  | 9  | AA778372 | AA778372 z156h05.s |
| c 35 | 415.8 | 38.8 | 419  | 9  | AA777994 | AA777994 z142c03.s |
| c 36 | 415   | 38.7 | 1013 | 11 | AK004091 | AK004091 Mus muscu |
| c 37 | 409.8 | 38.2 | 447  | 9  | AI199140 | AI199140 q146f11.x |
| c 38 | 406.8 | 37.9 | 1128 | 10 | BI413982 | BI413982 602991763 |
| c 39 | 395.4 | 36.9 | 403  | 9  | AA405247 | AA405247 UI-HF-BLO |
| c 40 | 394.4 | 36.8 | 397  | 9  | AI376136 | AI376136 la59c04.x |
| c 41 | 391.2 | 36.5 | 547  | 9  | AA749209 | AA749209 ny11h09.s |
| c 42 | 387.6 | 36.2 | 399  | 9  | AA236389 | AA236389 x015e01.x |
| c 43 | 382.6 | 35.7 | 872  | 10 | BI184046 | BI184046 UNL-D-FN- |
| c 44 | 379.2 | 35.4 | 423  | 10 | W47086   | W47086 zc43e03.r1  |
| c 45 | 377.4 | 35.2 | 524  | 10 | BE856755 | BE856755 7168c12.x |

## ALIGNMENTS

RESULT 1  
LOCUS AL543692 1011 bp mRNA linear EST 16-FEB-2001  
DEFINITION AL543692 LRT\_NFL006\_P12 Homo sapiens cDNA clone CS0DI006YD22 5  
prime, mRNA sequence.

ACCESSION AL543692  
VERSION AL543692.1 GI:12876171  
KEYWORDS EST.

## SOURCE

human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 1011)  
Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

## FEATURES

## source

## 1. 1011

## /organism="Homo sapiens"

## /db\_xref="taxon:9606"

## /clone="CS0DI006YD22"

## /clone\_lib="LRT\_NFL006\_P12"

## /issue\_type="placenta"

## /note="Vector: pCMVSPORT 6; site\_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end was enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifechem.com URL : http://fulllength.invitrogen.com"

## BASE COUNT

## ORIGIN

## 251 a

## 279 c

## 262 g

## 217 t

## 2 others

Query Match 90.0%; Score 964.8; DB 9; Length 1011;  
 Best Local Similarity 98.2%; Pred. No. 6.5e-227;  
 Matches 994; Conservative 2; Mismatches 14; Indels 2; Gaps 2;

QY 11 CCTCCGGAACAGCCATGGTGGCGGAGCGGTGGCAGCGCGTGGCTGCTCTGTGGGCT 70  
 DB 1 CCTCCGGAACAGCCATGGTGGCGGAGCGGTGGCAGCGCGTGGCTGCTCTGTGGGCT 60  
 QY 71 GCGGCGCTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 130  
 DB 61 GCGGCGCTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 119  
 QY 131 AAATGCTGTGCTGGAGAGATACCGGATGCGTGTCCGTGTGTAATGTGGCCAGC 190  
 DB 120 AAATGCTGTGCTGGAGAGATACCGGATGCGTGTCCGTGTGTAATGTGGCCAGC 179  
 QY 191 GAGTGGGCTTCCACAGACGAGCTACCGAGCCCTGAGAGCTGCAAGCAGAGCTGGGC 250  
 DB 180 GAGTGGGCTTCCACAGACGAGCTACCGAGCCCTGAGAGCTGCAAGCAGAGCTGGGC 239  
 QY 251 CCCGACCACTTCAAGTGTGCTGCTCCCTGCAACGAGTTTGCCCAACAGAGAGCTGAC 310  
 DB 240 CCCGACCACTTCAAGTGTGCTGCTCCCTGCAACGAGTTTGCCCAACAGAGAGCTGAC 299  
 QY 311 AGCAACAGAGAGATGAGAGCTTTGCTGCGGACCTACAGTGTCTCATTTCCCATGTTT 370  
 DB 300 AGCAACAGAGAGATGAGAGCTTTGCTGCGGACCTACAGTGTCTCATTTCCCATGTTT 359  
 QY 371 AGCAATTTGCACTACCGGTACTGTGTGCCATCTGCTTCAAGTACTGCGCCAGACT 430  
 DB 360 AGCAATTTGCACTACCGGTACTGTGTGCCATCTGCTTCAAGTACTGCGCCAGACT 419  
 QY 431 TCTGGGAAGAGGAGCCACTGGAATCTTGAAGTACTAGCCCAAGATGGAAGAGTG 490  
 DB 420 TCTGGGAAGAGGAGCCACTGGAATCTTGAAGTACTAGCCCAAGATGGAAGAGTG 479  
 QY 491 GTAGGGGCTTGGAGCCCACTGTGTCTAGTGGAGAGGTCTAGACTCCAGATCAGCGCTC 550  
 DB 480 GTAGGGGCTTGGAGCCCACTGTGTCTAGTGGAGAGGTCTAGACTCCAGATCAGCGCTC 539  
 QY 551 GTAGAGAGCTCATCTCTAGAGAGGAGAGAGAGTATTAACACCGGCTCTCTCTCCAC 610  
 DB 540 GTAGAGAGCTCATCTCTAGAGAGGAGAGAGTATTAACACCGGCTCTCTCTCCAC 599  
 QY 611 CACCTATCCCGCCCACTGTGTGGGCTGACCAATGCAACTCAATGCTGCTTCAAG 670  
 DB 600 CACCTATCCCGCCCACTGTGTGGGCTGACCAATGCAACTCAATGCTGCTTCAAG 659  
 QY 671 GGAGAGACCCACTGACTCTCTCTCTTACTTATGCAATGCTGCTTCTGTTG 730  
 DB 660 GGAGAGACCCACTGACTCTCTCTCTTACTTATGCAATGCTGCTTCTGTTG 719  
 QY 731 GGGGAAAAATTCATGATTTTGAATTTGAATCTTAACACAATAATAGAACTCTG 790  
 DB 720 GGGGAAAAATTCATGATTTTGAATTTGAATCTTAACACAATAATAGAACTCTG 779  
 QY 791 CCATGAG-AGCTCTGACAGTGAATCAGCAGCCGATGAGAGCTTGTCCAAACAAA 849  
 DB 780 CCATGAGAGCTCTTGTACAGTGAATCAGCAGCCGATGAGAGCTTGTCCAAACAAA 839  
 QY 850 TGTGTGGCAATAGAGTATATCAAGCAATATCTCCACCAAGGCTTGTGTAATGG 909  
 DB 840 TGTGTGGCAATAGAGTATATCAAGCAATATCTCCACCAAGGCTTGTGTAATGG 899  
 QY 910 GACCAATGATTAATAGAGGCTGTGTGAGATTAAGATGAATACCTGTGAAGTGC 969  
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RESULT 2  
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 DEFINITION  
 PRIMER, mRNA sequence.  
 ACCESSION  
 AL543655  
 VERSION  
 AL543655.1  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE  
 1 (bases 1 to 961)  
 Li, W.B., Gruber, C., Jesse, J., and Polayes, D.  
 TITLE  
 Full-length cDNA libraries and normalization  
 JOURNAL  
 Unpublished (2001)  
 COMMENT  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: [segreg@genoscope.cns.fr](mailto:segreg@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr),  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
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 /tissue\_type="placenta"  
 /note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA  
 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-stranded cDNA was digested with Not I and  
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
 vector. Library was normalized. Library was constructed by  
 Life Technologies. Contact : Feng Liang Life Technologies,  
 a division of Invitrogen 9800 Medical Center Drive  
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
 Email : [liang@life.com](mailto:liang@life.com) URL :  
<http://fulllength.invitrogen.com>

BASE COUNT 231 a 207 c 252 g 267 t 4 others  
 ORIGIN

Query Match 78.4%; Score 840.2; DB 9; Length 961;  
 Best Local Similarity 99.0%; Pred. No. 3.2e-196;  
 Matches 864; Conservative 2; Mismatches 5; Indels 2; Gaps 2;

QY 201 TCACAGACCAAGCTTACGAGCCCTGACAGAGCTGACGAGAGCTGAGGAGCTGAGGAGCT 260  
 DB 961 TCACAGACCAAGCTTACGAGCCCTGACAGAGCTGACGAGAGCTGAGGAGCTGAGGAGCT 902  
 QY 261 TCACAGCTGTGCGCTTCCCTGCAACCAAGTTTGCC-ACAGAGAGCTGACAGCAAG 319  
 DB 901 TCACAGCTGTGCGCTTCCCTGCAACCAAGTTTGCCCAACAGAGAGCTGACAGCAAG 842  
 QY 320 GAGATTGAGAGCTTGTGCTGCGGACCTACAGTGTCTCATTTCCCATGTTAGCAATT 379  
 DB 841 GAGATTGAGAGCTTGTGCGGACCTACAGTGTCTCATTTCCCATGTTAGCAATT 782  
 QY 380 GCAATGACCGGTACTGTGGCCATCTGCTTCAAGTACCTGGGCGAGAGCTTGGGAG 439  
 DB 781 GCAATGACCGGTACT-GTGGCCATCTGCTTCAAGTACCTGGGCGAGAGCTTGGGAG 723  
 QY 440 GAGCCCACTGGAATCTTGTGAAGTACCTGAGTACCCAGATGGAAGAGTGTAGGGCT 499  
 DB 722 GAGCCCACTGGAATCTTGTGAAGTACCTGAGTACCCAGATGGAAGAGTGTAGGGCT 663  
 QY 500 TGGAGCCCACTGTGTCAAGTGGAGAGGTCAAGCTCAGATCAGAGGCTGTGAGAGAG 559  
 DB 662 TGGAGCCCACTGTGTCAAGTGGAGAGGTCAAGCCAGATCAGAGGCTGTGAGAGAG 603  
 QY 560 CTATCTCTACTGAAGCAGAAAGACTTAAACACAGCGGTCTCTCTCCACACACCTCATC 619  
 DB 602 CTATCTCTACTGAAGCAGAAAGACTTAAACACAGCGGTCTCTCTCCACACACCTCATC 543



RESULT 4  
BI905842 936 bp mRNA linear EST 16-OCT-2001  
LOCUS 603062920F1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5212085 5',  
DEFINITION mRNA sequence.  
ACCESSION BI905842  
VERSION BI905842.1 GI:16168433  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 936)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLM11532 row: h column: 06  
High quality sequence start: 5  
High quality sequence stop: 861.  
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/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6; Site.1: NotI; Site.2: EcoRV  
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non-activated adult donors. Library is oligo-dT primed  
and directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.7 kb, insert size range  
1.2-3.3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 027. Note:  
this is a NIH\_MGC Library."  
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Best Local Similarity 91.9%; Pred. No. 6.9e-172;  
Matches 854; Conservative 0; Mismatches 56; Indels 19; Gaps 6;  
QY 13 TCCGGAACAAGCATTGTCGGCGACGGTGGCAGCGGCTGCTCTCTGGGCTGC 72  
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QY 73 GGCCTGCGGCGACGACGACGACTTCTACGACTCAAGGGGTCACATCCGGGCGAA 132  
DB 69 GGCCTGCGGCGACGACGACGACTTCTACGACTCAAGGGGTCACATCCGGGCGAA 128  
QY 133 ACTGCTGTGCTGAGAAATACCGCGATCGGTCTCTGTTGTAATGTGGCCAGCA 192  
DB 129 ACTGCTGTGCTGAGAAATACCGCGATCGGTCTCTGTTGTAATGTGGCCAGCA 188  
QY 193 GTGGGCTTTCACAGACCACTACCGAGCCCTGCAGACAGCTGCAGAGAGCTGGGCC 252  
DB 189 GTGGGCTTTCACAGACCACTACCGAGCCCTGCAGACAGCTGCAGAGAGCTGGGCC 248  
QY 253 CCACGACTTCAACGTCGCTGCTCCCTGTCACGACGATTGGCCACAGAGAGCTGACAG 312  
DB 249 CCACGACTTCAACGTCGCTGCTCCCTGTCACGACGATTGGCCACAGAGAGCTGACAG 308

QY 313 CAACAGAGAGATGTGAGACTTTGCTGCGCGACCTACAGTGTATCCCATGTTAG 372  
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QY 373 CAAGATTGCAGTACACCGGTACTGTGTGCCATCTGCTTCAAGTACCTGGCCACACTTC 432  
DB 369 CAAGATTGCAGTACACCGGTACTGTGTGCCATCTGCTTCAAGTACCTGGCCACACTTC 428  
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QY 493 AGGGGCTTGGGACCACTGTGTCAGTGGAGAGGTGACATCCAGATCACAGCGCTGT 552  
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DB 549 GAGGAGGCTCATCTACTGTAAGCGAAGACTTATTAACCAACCGGTCTCTCTCCACCA 608  
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DB 609 ACTCATCCCGCCACCTGTGTGGGGCTGACCAATGCAAACTGAATGGTCTTCAAGAG 668  
QY 673 AGAGACCCACTGACTCTCTCTCTTACTCTTATGCGCATTTGGTCC---CATCATTTCTTG 728  
DB 669 AGAGACCCACTGACTCTCTCTCTTACTCTTATGCGCATTTGGTCCCATTTCTTGTTG 728  
QY 729 TGGGGGAAATTTCTAG---TATTTGATTTATTTGAATCTTACAGCACAATAATAGAA 783  
DB 729 TGGGGGAAATTTCTAG---TATTTGATTTATTTGAATCTTACAGCACAATAATAGAA 788  
QY 784 ---CTCCGTGGCCAAATGAGAGCTCTT---GACCAGTGAATTCACAGCCGATAGAGCTGC 836  
DB 789 ACTCCCTGGCCAAATGAGAGCTCTT---GACCAGTGAATTCACAGCCGATAGAGCTGC 848  
QY 837 -TTGGCAACAAAATGTGTGGCAATAGAAATATCAAGTCAACAAATATCTCCACCAAG 895  
DB 849 TTGGCAACAAAATGTGTGGCAATAGAAATATCAAGTCAACAAATATCTCCACCAAG 908  
QY 896 CTTCCTTAACCTGGGACCAATGATTCCT 924  
DB 909 -TTCTGTAACTGGACCAATGATTCCT 935  
RESULT 5  
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LOCUS 603256131F1 NIH\_MGC\_97 Homo sapiens cDNA clone IMAGE:5298607 5',  
DEFINITION mRNA sequence.  
ACCESSION BI561449  
VERSION BI561449.1 GI:15448763  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 846)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (MHCRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLM11755 row: m column: 08





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VERSION      BI772530.1  GI:15764108
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1 (bases 1 to 720)
              NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE        Unpublished (1999)
JOURNAL      Contact: Robert Strausberg, Ph.D.
              Email: cga@b-remail.nih.gov
              Tissue Procurement: Life Technologies, Inc.
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://lmage.llnl.gov
              Plate: LLM11511 row: 9 column: 12
              High quality sequence start: 4
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              Location/Qualifiers
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    /db_xref="taxon:9606"
    /clone="IMAGE:5204003"
    /clone_lib="NIH_MGC_122"
    /lab_host="DH10B"
    /note="Organ: pooled lung and spleen; Vector: pCMV-Sport6;
    Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
    anonymous pool of 24 week female lung, 16 week female
    spleen, and 20-22 week male spleens. Library is oligo-dT
    primed and directionally cloned (EcoRV site is destroyed
    upon cloning). Average insert size 1.4 kb, insert size
    range 1-3 kb. Library is normalized and enriched for
    full-length clones and was constructed by C. Gruber
    (Invitrogen). Research Genetics tracking code 026. Note:
    this is a NIH-MGC Library."
BASE COUNT   150 a      225 c      204 g      141 t
ORIGIN
Query Match      61.0%; Score 653.6; DB 10; Length 720;
Best Local Similarity 98.8%; Pred. No. 2.7e-150;
Matches 711; Conservative 0; Mismatches 4; Indels 5; Gaps 5;

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Db 361 CCATGTTTAGCAAGATTGCTACCGGCTACTGCTGCCATCTGCTCAAGTACT 420
Qy 421 GGCCAGACTTCTGGAGAG-GAGCCACCTGGAACTTGTGAATCACTAGTACCCAG 479
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Qy 480 ATGG-AAAAGTGTAGAGGGCTTGGACCCAGCTGTGTCAGTGAAGAGTCAAGTCCAG 538
Db 481 ATGGTAAAGTGTAGAGGGCTTGGACCCAGCTGTGTCAGTGAAGAGTCAAGTCCAG 540
Qy 539 ATCAGAGCGCTGTGAGAGAGTCACTCTACTGAGAGAGTCAAGTCAAGTCAAGT 598
Db 541 ATCAGAGCGCTGTGAGAGAGTCACTCTACTGAGAGAGTCAAGTCAAGTCAAGT 600
Qy 599 CTCCTCTCCACACCTCATCTCCGCGCCAGCTGTGAGAGAGTCAAGTCAAGTCAAGT 658
Db 601 CTCCTCTCCACACCTCATCTCCGCGCCAGCTGTGAGAGAGTCAAGTCAAGTCAAGT 660
Qy 659 GGTGCTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 718
Db 661 GGTGCTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720

RESULT      9
AL554203/c 773 bp mRNA linear EST 16-FEB-2001
LOCUS       AL554203 LTI_NFL006.PL2 Homo sapiens cDNA clone CS0D1081YE05 3
DEFINITION prime, mRNA sequence.
ACCESSION   AL554203.1 GI:12894755
VERSION      AL554203.1
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1 (bases 1 to 773)
              Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
              Full-length cDNA libraries and normalization
              Unpublished (2001)
AUTHORS      Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 Evry cedex - France
              Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.
TITLE        Location/Qualifiers
JOURNAL
COMMENT
FEATURES
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    /clone_lib="LTI_NFL006_PL2"
    /tissue_type="placenta"
    /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
    was primed with a NotI-oligo(dT) primer. Five prime end
    enriched, double-stranded cDNA was digested with Not I and
    cloned into the Not I and Eco RV sites of the pCMVSPORT 6
    vector. Library was normalized. Library was constructed by
    Life Technologies. Contact : Feng Liang Life Technologies,
    a division of Invitrogen 9800 Medical Center Drive
    Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
    Email : fliang@lifetech.com URL :
    http://fulllength.invitrogen.com"
BASE COUNT   182 a      151 c      216 g      204 t      20 others
ORIGIN
Query Match      56.6%; Score 607; DB 9; Length 773;
Best Local Similarity 90.6%; Pred. No. 8.3e-139;
Matches 628; Conservative 12; Mismatches 53; Indels 0; Gaps 0;

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| Db         | 713   |
| Qy         | 500   |
| Db         | 653   |
| Qy         | 560   |
| Db         | 593   |
| Qy         | 620   |
| Db         | 533   |
| Qy         | 680   |
| Db         | 473   |
| Qy         | 740   |
| Db         | 413   |
| Qy         | 800   |
| Db         | 353   |
| Qy         | 860   |
| Db         | 293   |
| Qy         | 920   |
| Db         | 233   |
| Qy         | 980   |
| Db         | 173   |
| Qy         | 1040  |
| Db         | 113   |
| RESULT     | 10  |
| LOCUS      | BE383506  |
| DEFINITION | 60129858661 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628580 5', mRNA sequence.   |
| ACCESSION  | BE383506  |
| VERSION    | BE383506.1  |
| KEYWORDS   | EST.  |
| SOURCE     | human.  |
| ORGANISM   | Homo sapiens  |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.   |
| AUTHORS    | 1 (bases 1 to 617)  |
| TITLE      | NIH-MGC http://mgc.nci.nih.gov/   |
| JOURNAL    | National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1999)   |
| COMMENT    | Contact: Robert Strausberg, Ph.D.<br>Email: cga@bbs-remail.nih.gov<br>Tissue Procurement: ATCC<br>CDNA Library Preparation: Ling Hong/Rubin Laboratory<br>DNA Sequencing by: Incyte Genomics, Inc.<br>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov<br>Plate: LCM313 row: 1 column: 21<br>High quality sequence start: 7<br>High quality sequence stop: 617.<br>Location/Qualifiers<br>1..617 |

| Query Match               | Best Local Similarity   | Score  | DB  | Length |
|---------------------------|---|--------|-----|--------|
| Matches 602; Conservative | 99.7%; Pred. No. 2.6e-137;                                    | 600.8; | 10; | 617;   |
|                           | Mismatches 2; Indels 0; Gaps 0                                |        |     |        |
| 46                        | AGCGGCTGCTCTCTCTCTGCGCTCGCGCGCAGCAGCAGACTTTCACA               | 105    |     |        |
| 14                        | ACCGGGTGGCTCTCTCTGCGCTCGCGCGCAGCAGCAGACTTTCACA                | 73     |     |        |
| 106                       | CTTCAAGGGGTCACATCTCGGGGCAAACTGGTGTGCGAGAACTACCGGGATCGGT       | 165    |     |        |
| 74                        | CTTCAAGGGGTCACATCTCGGGGCAAACTGGTGTGCGAGAACTACCGGGATCGGT       | 133    |     |        |
| 166                       | GTCCCTGTGTGATGTGCGCCAGCGAGTGGCGCTTCACAGACAGCACTACGAGCCCT      | 225    |     |        |
| 134                       | GTCCCTGTGTGATGTGCGCCAGCGAGTGGCGCTTCACAGACAGCACTACGAGCCCT      | 193    |     |        |
| 226                       | GCAGCAGCTGCAGCGAGCTGGGGCCCACTCAACGTCTGCTCCCTCCGCA             | 285    |     |        |
| 194                       | GCAGCAGCTGCAGCGAGCTGGGGCCCACTCAACGTCTGCTCCCTCCGCA             | 253    |     |        |
| 286                       | CCAGTTTGGCCAAAGAGCCTGACAGCAAAAGAGATTGAGAGCTTCCCTGCGCAC        | 345    |     |        |
| 254                       | CCAGTTTGGCCAAAGAGCCTGACAGCAAAAGAGATTGAGAGCTTCCCTGCGCAC        | 313    |     |        |
| 346                       | CTACAGTGTCTATTCCTCCATGTGTAAGCAAGATTGCAGTACCGGTACTGTCCATCC     | 405    |     |        |
| 314                       | CTACAGTGTCTATTCCTCCATGTGTAAGCAAGATTGCAGTACCGGTACTGTCCATCC     | 373    |     |        |
| 406                       | TGCTCTCAAGTACTCTGCGCCACAGACTTCTGGGAAGAGCCACCTGGAACTTCTGGAAGTA | 465    |     |        |
| 374                       | TGCTCTCAAGTACTCTGCGCCACAGACTTCTGGGAAGAGCCACCTGGAACTTCTGGAAGTA | 433    |     |        |
| 466                       | CCTAGTAGCCCAATGGAAGGTGGTAGGGCTTGGGACCCCACTGTCTAGTGAAGA        | 525    |     |        |
| 434                       | CCTAGTAGCCCAATGGAAGGTGGTAGGGCTTGGGACCCCACTGTCTAGTGAAGA        | 493    |     |        |
| 526                       | GGTCAGACTCCAGATACAGCGCTGTGAGGAAGTCACTCTACTGAGGAGAGACTT        | 585    |     |        |
| 494                       | GGTCAGACTCCAGATACAGCGCTGTGAGGAAGTCACTCTACTGAGGAGAGACTT        | 553    |     |        |
| 586                       | ATAACACACCGCTCTCTCTCTCAGACACTCTCCCGCCACCTGTGTGGGCTGACCA       | 645    |     |        |
| 554                       | ATAACACACCGCTCTCTCTCTCAGACACTCTCCCGCCACCTGTGTGGGCTGACCA       | 613    |     |        |
| 646                       | TGCA 649  |        |     |        |
| 614                       | TGCA 617  |        |     |        |

RESULT 11

AL576668/c

LOCUS

DEFINITION

AL576668 LTI\_NFL006\_PL2 Homo sapiens cDNA clone CS0D1080YK02 3 prime, mRNA sequence.

ACCESSION

AL576668

907 bp

mRNA

linear

EST 16-FEB-2001

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:3628580"

/clone\_1ib="NIH\_MGC\_19"

/tissue\_type="neuroblastoma"

/lab\_host="PH10B (phage-resistant)"

/note="Organ: brain; Vector: pORF7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(6). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

BASE COUNT

130 a 193 c 178 g 116 t



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VERSION      AL576668.1    GI.:12939038
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS      Li,W.B., Gruber,C.J., Jesse,J. and Polayes,D.
TITLE        Full-length cDNA libraries and normalization
JOURNAL      Unpublished (2001)
COMMENT       Contact : Genoscope
               Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.
FEATURES
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           /db_xref="taxon:9606"
           /clone="CSDDI080YK02"
           /clone_id="LTL_NFLD06_PL2"
           /lsize_type="placenta"
           /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand CDNA was primed with a NotI-oliigo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT   309 a            88 c          219 g         251 t             40 others
ORIGIN
Query Match      51.9%; Score 556.2; DB 9; Length 907; Best Local Similarity 87.6%; Pred.No.2.9e-126; Matches 567; Conservative 31; Mismatches 49; Indels 0; Gaps 0;
QY  426 AGACTCTCGGAGAGACCCCACTGTGAATCCTGGAACTTAGCCCCAGATGGNA 485
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Db  751 ATACTCTTTTAATTATTCACCACCTTACTCTTTAATTACTATAATCCCATTNTNA 692
QY  486 AAGTGGAAGGCCCTTGGACCCAAGTGTGCATGAGAGAAGGTGCACTCCAGATCACG 545
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Db  691 ATTTTTTTTTCTTTTACCACAAGTTTCTTATTATTAKTYCAKACCCCATTCACAK 632
QY  546 CGCTCGTAGGAGAGCTACTCTACTGAAAGCGAAGAGACTTAAACCACCGCTCTCC 605
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Db  631 CTCCTCTTAKTNATCTCATCCACTTAATCYARAKAKCTTATMAACCGCKTCTCC 572
QY  606 TCCACACCTCATFCCCGGCCAACCTGTGGGGGTGACCAATGCAAATCAATGGTGCT 665
      ||||| | | | | | | | | | | | | | | | | | | | | |
Db  571 TTCACACACTCATCCCGGCCACACCTTKTRKKRKTACCAATGCAATCAATCAATGCT 512
QY  666 CAAGGGAAGACCCCACTGACTCTCTCTCTCTTACTCTTANGCAATTGGTCCCATATTC 725
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Db  511 CAAAAGGAGAGACCCCACTGACTCTCTCTCTCTTACTCTTANGCAATTGGTCCCATATTC 452
QY  726 TTGTGGGGGAAAAAATTCTAGTATTTTGTATTTTGAATCTTACAGCAAAATAGGA 785
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Db  451 TTKTKGGGAAAAAATTCTWKMTATTTTGTATTTTGAATCTTACAGCAAAATAGGA 392
QY  786 CCTGGCAATGAGACTCTTGACACAGTAAATACACGCGATGAGAGACTCTTGCAACA 845
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Db  391 CCTGGCAATRAAGACYCTTGACACAGTAAATMCMCGCGACACGAAGACTCTTGCGMACA 332
QY  846 AAAATGTGTGGCAATAGAAATATATCAAGCAATATCTCCACCCAAAGGCTTGTANA 905
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Db  331 AAATRTKTGGCAATAGAAATATATCAAGCAATATCTCCACCCAAAGGCTTGTANA 272
QY  906 CTGGGACCAATGATTACTCATAGGGCGTGTGTGAGGATTAGATGAATTAACCTGTGAAA 965

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| Db                        | 271  | CTGGAGCAATGATTACCTCAATGAGGCGTGTGTGAGAGATTAGATGAAATACGTGTGAA     | 212                         |
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| QY                        | 966  | GTGCGCTTAGCAGTGTCCAGCCAAATAGAGGCGCATTCATGAACATTTTTCATATATAAC    | 1025                        |
| Db                        | 211  | GTGCGCTTAGCAGTGTCCAGCCAAATAGAGGCGCATTCATGAACATTTTTCATATATAAC    | 152                         |
| QY                        | 1026   | AAAAAATACCTGTATCAATATAAAACCTGCATCCAACTGAATTTTC                  | 1072                        |
| Db                        | 151  | AAAAAATACCTGTATCAATATAAAACCTGCATCCAACTGAATTTTC                  | 105                         |
| RESULT                    | 12   |   |                             |
| LOCUS                     | AM957082   | 625 bp  | mRNA linear EST 01-JUN-2000 |
| DEFINITION                | EST369152 MAGE resequences, MAGD Homo sapiens cDNA, mRNA sequence.   |   |                             |
| ACCESSION                 | AM957082   |   |                             |
| VERSION                   | AM957082.1   | GI:8146765  |                             |
| KEYWORDS                  | EST.   |   |                             |
| SOURCE                    | human.   |   |                             |
| ORGANISM                  | Homo sapiens   |   |                             |
| REFERENCE                 | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.                          |   |                             |
| ATTN                      | 1 (bases 1 to 625)   |   |                             |
| REFERENCE                 | Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Seed, A.I., Sharov, V., Lee, N.H., Teatman, T.J. and Quackenbush, J. |   |                             |
| REFERENCE                 | Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray unpublished (2000)                |   |                             |
| REFERENCE                 | Contact: John Quackenbush  |   |                             |
| REFERENCE                 | The Institute for Genomic Research   |   |                             |
| REFERENCE                 | 9712 Medical Center Dr., Rockville, MD 20850, USA  |   |                             |
| REFERENCE                 | Tel: 301 838 3528  |   |                             |
| REFERENCE                 | Fax: 301 838 0208  |   |                             |
| REFERENCE                 | Email: jhohnq@tigr.org   |   |                             |
| REFERENCE                 | Plate: 101   |   |                             |
| REFERENCE                 | Seq primer: Reverse.   |   |                             |
| REFERENCE                 | Location/Qualifiers  |   |                             |
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| REFERENCE                 | /clone_lib="MAGE resequences, MAGD"  |   |                             |
| REFERENCE                 | /note="Vector: p Bluescriptskm"  |   |                             |
| REFERENCE                 | 200 a 150 c 127 g 147 t 1 others   |   |                             |
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| ORIGIN                    |  |   |                             |
| Query Match               | 51.88;   | Score 555.8;  | DB 9; Length 625;           |
| Best Local Similarity     | 99.68;   | Prod. No. 3.2e-126;   |                             |
| Matches 557; Conservative | 0;   | Mismatches 2;   | Indels 0; Gaps 0;           |
| QY                        | 514  | GTCAAGTGGAGAGGTGCACACTCCAGATACAGAGCGCTGTGAGAACTCATCTACTGAA      | 573                         |
| Db                        | 1  | GTCAAGTGGAGAGGTGCACAGCCCGCAGATACAGCGCTGTGAGAACTCATCTACTGAA      | 60                          |
| QY                        | 574  | GCGAGAAAGACTTATTAACCAACGCGCTCTCTCTCCACACCTCATCCGCCACCTGTGT      | 633                         |
| Db                        | 61   | GCGAGAAAGACTTATTAACCAACGCGCTCTCTCTCCACACCTCATCCGCCACCTGTGT      | 120                         |
| QY                        | 634  | GGGGCTGACCAATGCAAACTCAATGGTGTCTTCAAAAGGAGAGAGACCCACTGACTCTCTT   | 693                         |
| Db                        | 121  | GGGGCTGACCAATGCAAACTCAAAATGGTGTCTTCAAAAGGAGAGAGACCCACTGACTCTCTT | 180                         |
| QY                        | 694  | CCTTACCTTATGACCATTTGGTCCCATCTCTTGTGGGGGAAAAATCTAGTATTTTGA       | 753                         |
| Db                        | 181  | CCTTACCTTATGACCATTTGGTCCCATCTCTTGTGGGGGAAAAATCTAGTATTTTGA       | 240                         |
| QY                        | 754  | TTATTTGAATCTTACAGCAACAATAGAACTCTGTGGCAATGAGAGCTTTGACCAAGTG      | 813                         |
| Db                        | 241  | TTATTTGAATCTTACAGCAACAATAGAACTCTGTGGCAATGAGAGCTTTGACCAAGTG      | 300                         |
| QY                        | 814  | AATCAACGCGCGATTCGAAAGCTTTGGCAACAAAAATGTGTGGCAATGAGAGTATATCA     | 873                         |

Db 301 AATCACCAGCCGATACGACGCTTGGCCAAACAAATGTGTGGCAATAGAGTATATCA 360  
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Qy 934 GTTGTGAGATTTAGATGAATATACCTGTGAAGTGCCTAGACAGTGCACCAATAGGA 993  
Db 421 GTTGTGAGATTTAGATGAATATACCTGTGAAGTGCCTAGACAGTGCACCAATAGGA 480  
Qy 994 GGCATTAAATGACATTTTTCATATAAACCAAAAAATTAATCTTTATCAATAAAACT 1053  
Db 481 GGCATTAAATGACATTTTTCATATAAACCAAAAAATTAATCTTTATCAATAAAACT 540  
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Db 541 TGCATTCACATGATTTTC 559

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LOCUS BE314194 534 bp mRNA linear EST 26-OCT-2000  
DEFINITION 601152806F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:3509112 5',  
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ACCESSION BE314194  
VERSION BE314194  
KEYWORDS GI:9135018  
SOURCE EST.  
ORGANISM human.  
Hom sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 534)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapds-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: Image.Lnl.gov  
Plate: LLM191 row: K column: 01  
High quality sequence stop: 534.  
Location/Qualifiers  
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/tissue\_type="neuroblastoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: brain; Vector: pORF7; Site: 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

BASE COUNT 111 a 161 c 165 g 97 t  
ORIGIN

Query Match 49.5%; Score 530.8; DB 10; Length 534;  
Best Local Similarity 99.6%; Pred. No. 4.3e-120;  
Matches 532; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 18 AACAGCCATGTGTGGCGGACGAGCGGCGGTGCTCCGTGGCGGCGGCGCT 77  
Db 1 AACAGCCATGTGTGGCGGACGAGCGGCGGTGCTCCGTGGCGGCGGCGCT 60

Qy 78 GCGGAGACGAGGACGAGACTTCTACAGCTTCAAGGCGGTCAACATCCGGGCAAACTGG 137  
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Qy 198 GCTTCACAGACGACACTACCGACGCTTGCAGCAGCTGCAGCAGACCTGGGCCCCACC 257  
Db 181 GCTTCACAGACGACACTACCGACGCTTGCAGCAGCTGCAGCAGACCTGGGCCCCACC 240  
Qy 258 ACTTCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 317  
Db 241 ACTTCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
Qy 318 AGGAGATTGAGACTTTCCTGCGGACCTACAGTGTCTATTCCTCCATGTTTGGCAGA 377  
Db 301 AGGAGATTGAGACTTTCCTGCGGACCTACAGTGTCTATTCCTCCATGTTTGGCAGA 360  
Qy 378 TTGCACTACACCGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 437  
Db 361 TTGCACTACACCGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
Qy 438 AGGAGCCACCTGGAATCTGTGAGAGTACCTAGTACCCAGATGGAAGGTGTAGGGG 497  
Db 421 AGGAGCCACCTGGAATCTGTGAGAGTACCTAGTACCCAGATGGAAGGTGTAGGGG 480  
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Db 481 CTTGGGACCCCACTGTGTCTAGTGTGAGAGTGTGAGTCCAGATCAGACGCGCTGG 534

RESULT 14  
LOCUS AW959644 542 bp mRNA linear EST 01-JUN-2000  
DEFINITION EST371714 MAGE resequences, MAGF Homo sapiens cDNA, mRNA sequence.  
ACCESSION AW959644  
VERSION AW959644.1 GI:8149328  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 542)  
Hedge, P., Qi, R., Abernathy, K., Dharap, S., Gaspar, R., Gay, C., Holt  
, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and  
Quackenbush, J.  
Assessment of gene expression patterns in a model of colon tumor  
metastasis using a 19,200 element cDNA microarray  
Unpublished (2000)  
Contact: John Quackenbush  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 3528  
Fax: 301 838 0208  
Email: johnq@ligr.org  
Plate: 135  
Seq primer: Forward.  
Location/Qualifiers  
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/organism="Homo sapiens"  
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/clone\_image="MAGE resequences, MAGF"  
/note="Vector: pBluescriptSm"

JOURNAL  
COMMENT

FEATURES  
source

BASE COUNT 117 a 161 c 161 g 103 t  
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Query Match 47.6%; Score 510.8; DB 9; Length 542;  
Best Local Similarity 97.6%; Pred. No. 3.7e-115;  
Matches 529; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

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QY 102 AGCAGTTCAAGGCGGTGCAACATCCGGGCAAACTGCTGTGAGAGAGTACC GGAT 161
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Db 61 ACAGACTTCAAGGCGGTGCAACATCCGGGCAAACTGCTGTGAGAGAGTACC GGAT 120
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QY 162 CGGTGCTCCGTGGTGAATGTGGCCAGGAGTGGGCTTACAGACACACTACCGAG 221
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Db 121 CGGCGTCCGTGGTGAATGTGGCCAGGAGTGGGCTTACAGACACACTACCGAG 180
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Db 181 CCGTGAGAGAGCTGACGAGAGAGTGGGCGCCACCACTTCAACGTCCTCCCT 240
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QY 282 GCACACAGTTGGCCAAACAGAGAGCTGACAGCAACAGAGAGTGGGCTTCCCTGCC 341
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Db 241 GCACACAGTTGGCCAAACAGAGAGCTGACAGCAACAGAGAGTGGGCTTCCCTGCC 300
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Db 361 ATCTGCTCTCAAGTACGTCGCGCCAGACTTCTGGAGAGAGAGCCACTGTGACTTGA 420
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QY 521 GAGGAGGTGAGACTGAGATCAACAGCGCTGAGAGAGCTCATCTACTGAAGCGAGAA 580
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QY 581 GA 582
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Db 541 GA 542
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RESULT 15
AA006605/c 519 bp mRNA linear EST 17-MAY-1997
LOCUS zvlb04.s1 Soares_NhMpu_S1 Homo sapiens cDNA clone IMAGE:753679
DEFINITION 3', mRNA sequence.
ACCESSION AA006605
VERSION AA006605
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 519)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisler,G., Jost,S.,
Kucaba,T., Lacey,M., Le,N., Lennon,G., Merra,M., Martin,J., Moore,B.,
Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
TITLE JOURNAL
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estelw@wustl.edu
This clone is available royalty-free through LNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m3 fwd. ET from Amersham
High quality sequence stop: 461.
Location/Qualifiers
1..519
/organism="Homo sapiens"

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/db_xref="GDB:5976543"
/db_xref="taxon:9606"
/clone="IMAGE:753679"
/clone_lib="Soares_NhMpu_S1"
/clisue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/clone_host="Dh10B"
/clone_note="Organ: mixed (see below); Vector: pT73D-Pac
(pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NDHM, pregnant uterus
NbHpu, and fetal heart NbH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of 1.N.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
BASE COUNT 131 a 100 c 126 g 162 t
ORIGIN

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Query Match 47.6%; Score 510.4; DB 9; Length 519;
Best Local Similarity 99.8%; Pred. No. 4.5e-115;
Matches 511; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 556 GAAGCTCATCTCTAGTGAAGAGAGACTTATACACCGGCTCTCTCCACCACT 615
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Db 512 GAACTCATCTCTAGTGAAGAGAGACTTATACACCGGCTCTCTCCACCACT 453
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QY 616 CATCCCGCCCACTGTGTGGGGCTGACCAATGCAAACTCAATGTGCTTCAAGGAGA 675
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Db 452 CATCCCGCCCACTGTGTGGGGCTGACCAATGCAAACTCAATGTGCTTCAAGGAGA 393
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QY 676 GACCCACTGACTCTCTCTCTTACTCTTATGCAATGTGTCCTTCTTGGGGGA 735
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Db 92 AGTGCCAGCAATATAGAGGCAATCAATGAAATTTTGGATTAATCAACCAATAATPAC 33
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Job time: 6879 sec

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